AMENDMENTS TO THE SPECIFICATION

On page 1, before the heading "FIELD" (i.e., before line 3) please add the following paragraph:

-- This application is the National Stage of International Application No. PCT/EP2004/006887, filed on June 25, 2004. --

Please replace the paragraph beginning at line 19 on page 6 of the specification with the following amended paragraph:

-- A modified human TPO molecule having the formula / structure (M)

SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGX^1X^2KTQX^3EEX^4KX^5X^6DX^7LGAX^8T X^9L$X^{10}X^{11}$GVMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK VRFLMLVGGSTLCVRRAPPTTA$X^{12}X^{13}$SRTSLVLTLNEL (SEQ ID NO: 1), wherein

X^1 is A, E;

X^2 is S, W;

X^3 is A or T or K, S or M;

X^4 is A, T;

X^5 is R, A;

X^6 is A or T or Q;

X^7 is A or T or I;

X^8 is A or T or V;

X^9 is A or T or S or L;

X^{10} is A or L;

X^{11} is A or S or E;

X^{12} is N or A or T or R or E or D or G or H or P or K or Q or V;

X^{13} is A or P,

and whereby simultaneously X^1 = E, X^2 = W, X^3 = M, X^4 = T, X^5 = A, X^6 = Q, X^7 = I, X^8 = V, X^9 = L, X^{10} = L, X^{11} = E, X^{12} = V and X^{13} = P are excluded, said meanings representing the native human TPO. --

Please replace the paragraph beginning at line 23 on page 7 of the specification with the following amended paragraph:

-- A fusion protein as specified, wherein said TPO portion has the formula / structure (M):

SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGX^1X^2KTQX^3EEX^4KX^5X^6DX^7LGAX^8T X^9L$X^{10}X^{11}$GVMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK VRFLMLVGGSTLCVRRAPPTTA$X^{12}X^{13}$SRTSLVLTLNEL (SEQ ID NO: 1), wherein

X^1 is A, E;

X^2 is S, W;

X^3 is A or T or K, S or M;

X^4 is A, T;

X^5 is R, A;

X^6 is A or T or Q;

X^7 is A or T or I;

X^8 is A or T or V;

X^9 is A or T or S or L;

X^{10} is A or L;

X^{11} is A or S or E;

X^{12} is N or A or T or R or E or D or G or H or P or K or Q or V;

X^{13} is A or P,

and whereby simultaneously X^1 = E, X^2 = W, X^3 = M, X^4 = T, X^5 = A, X^6 = Q, X^7 = I, X^8 = V, X^9 = L, X^{10} = L, X^{11} = E, X^{12} = V and X^{13} = P are excluded. --

Please replace the paragraph beginning at line 24 on page 8 of the specification with the following amended paragraph:

-- A peptide molecule selected from the group consisting of

GEWKTQMEETKAQDILGAVTLLLEGVM (SEQ ID NO: 2),

PTTAVPSRTSLVLTL (SEQ ID NO: 3);

or a sequence track consisting of at least 9 consecutive amino acid residues of any of said peptide molecules having a potential MHC class II binding activity and created from the primary sequence of non-modified human TPO in its truncated form (1 – 174), whereby said peptide molecule or

sequence track has a stimulation index of > 1.8 in a biological assay of cellular proliferation and said index is taken as the value of cellular proliferation scored following stimulation by a peptide and divided by the value of cellular proliferation scored in control cells not in receipt peptide and wherein cellular proliferation is measured by any suitable means. --

Please replace the paragraph beginning at line 3 on page 10 of the specification with the following amended paragraph:

-- In nature, the mature TPO protein is single polypeptide of 332 amino acids The amino acid sequence of TPO (depicted as single-letter code) is as follows (M68):

SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGEWKTQMEETKAQDILGAVTLLLEG
VMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVG
GSTLCVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKWQQGFRAKIPGLLNQTSRSL
DQIPGYLNRIHELLNGTRGLFPGPSRRTLGAPDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTL
PTPVVQLHPLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG (SEQ ID NO: 4). --

Please replace the paragraph beginning at line 9 on page 12 of the specification with the following amended paragraph:

-- A "linker" or "linker peptide" refers herein to a peptide segment joining two moieties of fusion protein. An example of a linker peptide is provided by the amino acid sequence $(G)_4S(G)_4S(G)_3SG$ (SEQ ID NO: 5). However, also other linker peptides, preferably having 4 – 20 amino acid residues can be used according to the invention. The fusion proteins of the present invention contain such a linker but not all fusion proteins contain a linker. --

Please replace the paragraph beginning at line 15 on page 16 of the specification with the following amended paragraph:

-- The major embodiments of the present invention are encompassed by the TPO protein sequences M1 – M67 and the fusion protein sequences F – M1 to F – M 67, or F – L – M1 to F – L – M67, or F1 – L1 – M1 to F1 – L1 – M67. The proteins are fusion proteins of the type "Fc-X" wherein X in this present instance comprise TPO muteins. The TPO proteins are expressed in mammalian cell-lines as a C-terminal fusion partner, linked to the Fc unit of human IgG_4. The TPO sequence is fused preferably to the C-terminus of a hinge modified/C_H2/C_H3 Fc region of human

IgG_4 via a 15 amino acid flexible linker between the C-terminus of the C_H3 and the N-terminus of TPO. The TPO domain comprises only residues 1-174 of the native counterpart. The amino acid sequence of the linker was as follows: $(G)_4S(G)_4S(G)_3SG$ (SEQ ID NO: 5). The expressed fusion protein had a stoichiometry of (hinge-C_H2-C_H3-linker-$TPO_{(1-174)})_2$. --

Please replace the paragraph beginning at line 28 on page 18 of the specification with the following amended paragraph:

-- Two epitope regions were identified in these studies. Region 1 encompasses TPO residues 49 – 75 and comprises the sequence: GEWKTQMEETKAQDILGAVTLLLEGVM (SEQ ID NO: 2). Region 2 encompasses TPO residues 157 – 171 and comprises the sequence: PTTAVPSRTSLVLTL (SEQ ID NO: 3). --

Please replace the paragraph beginning at line 5 on page 20 of the specification with the following amended paragraph:

-- Taken together, the inventors have been able to define improved TPO proteins which can be depicted by the following structure (M):

SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGX^1X^2KTQX^3EEX^4KX^5X^6DX^7LGAX^8T X^9L$X^{10}X^{11}$GVMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK VRFLMLVGGSTLCVRRAPPTTA$X^{12}X^{13}$SRTSLVLTLNEL (SEQ ID NO: 1), wherein

X^1 is A, E;

X^2 is S, W;

X^3 is A or T or K, S or M;

X^4 is A, T;

X^5 is R, A;

X^6 is A or T or Q;

X^7 is A or T or I;

X^8 is A or T or V;

X^9 is A or T or S or L;

X^{10} is A or L;

X^{11} is A or S or E;

X^{12} is N or A or T or R or E or D or G or H or P or K or Q or V;

X^{13} is A or P,

and whereby simultaneously X^1 = E, X^2 = W, X^3 = M, X^4 = T, X^5 = A, X^6 = Q, X^7 = I, X^8 = V, X^9 = L, X^{10} = L, X^{11} = E, X^{12} = V and X^{13} = P are excluded,

or, alternatively, fusion proteins of the structure:

$$F - (L)n - M,$$

wherein M has the meaning as specified above, F is an immunoglobulin heavy chain constant region, preferably an Fc portion, and L is an optional linker molecule (n = 0, 1), preferably a peptide linker having 4 – 20 amino acid residues. Preferably the Fc region derives from human IgG4 an may be linked at its N-terminal to a hinge region, which may be modified in order to reduce immunogenicity or to improve other desired properties. --

Please replace the paragraph beginning at line 7 on page 21 of the specification with the following amended paragraph:

-- To aid the understanding of the invention, Table 1 below sets out a description of the fusion protein TPO muteins. The derivation and properties of these proteins are also more fully disclosed in the examples. In Table 1 the column heading labeled "Substitution(s)" refers to substitutions in SEQ ID NO: 4, i.e., native human TPO. --

Please replace the Table A1, beginning at the line labeled "6" on page 23 and extending through line 17 on page 32 with the following amended table:

-- M1 – M67 (modified human TPO, truncated form 1 – 174)

M1 (SEQ ID NO: 6):

```
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K R Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L
```

M2 (SEQ ID NO: 7):

```
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
```

T L C V R R A P P T T A N A S R T S L V L T L N E L

M3 (SEQ ID NO: 8):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A N A S R T S L V L T L N E L

M 4 (SEQ ID NO: 9):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q A E E T K A Q D A L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M5 (SEQ ID NO: 10):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q T E E T K A Q D A L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M6 (SEQ ID NO: 11):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q T E E T K A Q D T L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M7 (SEQ ID NO: 12):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A A D A L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M8 (SEQ ID NO: 13):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A A D T L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M9 (SEQ ID NO: 14):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M10 (SEQ ID NO: 15):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M11 (SEQ ID NO: 16):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M12 (SEQ ID NO: 17):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M13 (SEQ ID NO: 18):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M14 (SEQ ID NO: 19):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A R P S R T S L V L T L N E L

M15 (SEQ ID NO: 20):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K M Q M E E T K A Q D I L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M16 (SEQ ID NO: 21):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M17 (SEQ ID NO: 22):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M18 (SEQ ID NO: 23):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M19 (SEQ ID NO: 24):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A E P S R T S L V L T L N E L

M20 (SEQ ID NO: 25):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M21 (SEQ ID NO: 26):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A R P S R T S L V L T L N E L

M22 (SEQ ID NO: 27):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A E P S R T S L V L T L N E L

M23 (SEQ ID NO: 28):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M24 (SEQ ID NO: 29):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M25 (SEQ ID NO: 30):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M26 (SEQ ID NO: 31):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M27 (SEQ ID NO: 32):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M28 (SEQ ID NO: 33):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A E P S R T S L V L T L N E L

M29 (SEQ ID NO: 34):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A R P S R T S L V L T L N E L

M30 (SEQ ID NO: 35):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M31 (SEQ ID NO: 36):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G A W K T Q M E E T K A Q D I L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M32 (SEQ ID NO: 37):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G A W K T Q M E E T K A Q D A L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M33 (SEQ ID NO: 38):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G A W K T Q M E E T K A Q D T L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M34 (SEQ ID NO: 39):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G A W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A E P S R T S L V L T L N E L

M35 (SEQ ID NO: 40):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L

M36 (SEQ ID NO: 41):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A D P S R T S L V L T L N E L

M37 (SEQ ID NO: 42):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A E P S R T S L V L T L N E L

M38 (SEQ ID NO: 43):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A G P S R T S L V L T L N E L

M39 (SEQ ID NO: 44):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A H P S R T S L V L T L N E L

M40 (SEQ ID NO: 45):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A N P S R T S L V L T L N E L

M41 (SEQ ID NO: 46):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A P P S R T S L V L T L N E L

M42 (SEQ ID NO: 47):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A K P S R T S L V L T L N E L

M43 (SEQ ID NO: 48):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A Q P S R T S L V L T L N E L

M44 (SEQ ID NO: 49):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A R P S R T S L V L T L N E L

M45 (SEQ ID NO: 50):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A T P S R T S L V L T L N E L

M46 (SEQ ID NO: 51):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A A T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M47 (SEQ ID NO: 52):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A T T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M48 (SEQ ID NO: 53):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D A L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M49 (SEQ ID NO: 54):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D T L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M50 (SEQ ID NO: 55):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A A D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M51 (SEQ ID NO: 56):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A T D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M52 (SEQ ID NO: 57):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q A E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M53 (SEQ ID NO: 58):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q K E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M54 (SEQ ID NO: 59):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q S E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M55 (SEQ ID NO: 60):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q T E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M56 (SEQ ID NO: 61):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E A K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M57 (SEQ ID NO: 62):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E S K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M58 (SEQ ID NO: 63):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G A W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M59 (SEQ ID NO: 64):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T A L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M60 (SEQ ID NO: 65):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T S L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M61 (SEQ ID NO: 66):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T T L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M62 (SEQ ID NO: 67):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L A E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M63 (SEQ ID NO: 68):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L A G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M64 (SEQ ID NO: 69):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L S G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M65 (SEQ ID NO: 70):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K R Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M66 (SEQ ID NO: 71):

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q K E E T K R Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L

M67 (SEQ ID NO: 72):
S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q K E E T K R Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A A P S R T S L V L T L N E L --

Please replace Table A2 beginning at line 21 on page 32 with the following amended table:

-- M68 (wild-type human TPO, truncated form 1 – 174)

S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T
P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G V
M A A R G Q L G P T C L S S L L G Q L S G Q V R L L L G A L Q S L L G T Q
L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S
T L C V R R A P P T T A V P S R T S L V L T L N E L (SEQ ID NO: 4). --

Please replace Table A3 beginning at line 30 on page 32 with the following amended table:

-- F1 (Fc domain of human IgG4 including modified hinge region)

E P K S S D K T H T C P P C P A P E F L G G P S V F L F P P K P K D T L M
I S R T P E V T C V V V D V S Q E D P E V Q F N W Y V D G V E V H N A K T
K P R E E Q F N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K
G L P S S I E K T I S K A K G Q P R E P Q V Y T L P P S Q E E M T K N Q V
S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S
D G S F F L Y S K L T V D K S R W Q Q G N I F S C S V M H E A L H N H Y T
Q K S L S L S P G A (SEQ ID NO: 73). --

Please replace Table A4 beginning at line 42 on page 32 with the following amended table:

-- L1 (Linker peptide)

G G G G S G G G G S G G G S G (SEQ ID NO: 5). --

Please replace the paragraph beginning at line 4 on page 34 of the specification with the following amended paragraph:

-- Identification of T cell epitopes in TPO (1-174). (A) 20 healthy donors were tested for reactivity with 55 overlapping (by 12 amino acids) 15mer peptides derived from the TPO sequence. Donors that responded to peptides with an SI>2 were analyzed further by plotting the frequency of donor responses to each peptide. Prominent regions of immunogencity are labelled according to the amino acid residue number in the TPO linear sequence and were determined by peptides that induced responses in 10% of donors; however, borderline responses where individual SI values >1.95 (hatched bars) were achieved and if two (or more) adjacent peptides induced responses in 5% of donors (Region 1). (B) The mature sequence of TPO (SEQ ID NO: 4) with regions of immunogenicity boxed and highlighted in bold. --

Please replace the paragraph beginning at line 5 on page 35 of the specification with the following amended paragraph:

-- The modified TPO proteins of the present invention were made using conventional recombinant DNA techniques. The N-terminal domain of the protein was cloned comprising residues 1-174. The coding sequence for TPO (1-174) was cloned from human human liver cDNA library using PCR. The wild-type gene was used both as a control reagent and a template from which to derive modified TPO proteins by site directed mutagenesis. WT and modified genes were inserted into a modified version of the expression vector pdC-huFc [~~Lo K-M et al, (1998) *Protein Eng* 11:495-500~~ K.-M. Lo et al., (1998) *Protein Eng.* 11:495-500]. The TPO gene was excised with *Xma*I and *Xho*I and cloned into a similarly cut preparation of the vector which had been modified such that the TPO sequence is fused to the C-terminus of a hinge modified/C_H2/C_H3 Fc region of human IgG_4 via a 15 amino acid flexible linker between the C-terminus of the C_H3 and the N-terminus of $TPO_{(1-174)}$. The amino acid sequence of the linker was as follows: $(G)_4S(G)_4S(G)_3SG$ (SEQ ID NO: 5). The expressed fusion protein had a stoichiometry of (hinge-C_H2-C_H3-linker-$TPO_{(1-174)})_2$. The final construct used in this study was designated Fc-gamma 4-linker-TPO (clone ID 00, M68 /F1-L1-M68). --

Please replace the paragraph beginning at line 24 on page 37 of the specification with the following amended paragraph:

-- A total of 67 different TPO variants demonstrated positive activity in the proliferation assay. Positive activity was taken to be a relative activity value of less than 10. Relative activity was determined by dividing the ED_{50} value derived for the protein of interest by the ED_{50} value derived for the control (WT) TPO fusion protein (M66/F1-L1-M66). Of these active proteins, 31 were muteins comprising a single amino acid substitution; 23 comprised 2 amino acid substitutions, 7 comprised 3 amino acid substitutions and 7 comprised four amino acid substitutions. The sequence of each of these active TPO muteins is provided in M1 - M67 (F1-L1-M67). The relative activities of each functioning mutein are provided in Table 2. In Table 2, the heading labled "Substitution(s)" refers to an amino acid residue substitution in SEQ ID NO: 4 (human TPO). --

Please replace Table 3 beginning after line 20 on page 40 with the following amended table:

Peptide No	Peptide sequence	SEQ ID NO:	Peptide No	Peptide sequence	SEQ ID NO:
1	SPAPPACDLRVLSKL	74	29	CLSSLLGQLSGQVRL	102
2	PPACDLRVLSKLLRD	75	30	SLLGQLSGQVRLLLG	103
3	CDLRVLSKLLRDSHV	76	31	GQLSGQVRLLLGALQ	104
4	RVLSKLLRDSHVLHS	77	32	SGQVRLLLGALQSLL	105
5	SKLLRDSHVLHSRLS	78	33	VRLLLGALQSLLGTQ	106
6	LRDSHVLHSRLSQCP	79	34	LLGALQSLLGTQLPP	107
7	SHVLHSRLSQCPEVH	80	35	ALQSLLGTQLPPQGR	108
8	LHSRLSQCPEVHPLP	81	36	SLLGTQLPPQGRTTA	109
9	RLSQCPEVHPLPTPV	82	37	GTQLPPQGRTTAHKD	110
10	QCPEVHPLPTPVLLP	83	38	LPPQGRTTAHKDPNA	111
11	EVHPLPTPVLLPAVD	84	39	QGRTTAHKDPNAIFL	112
12	PLPTPVLLPAVDFSL	85	40	TTAHKDPNAIFLSFQ	113
13	TPVLLPAVDFSLGEW	86	41	HKDPNAIFLSFQHLL	114
14	LLPAVDFSLGEWKTQ	87	42	PNAIFLSFQHLLRGK	115
15	AVDFSLGEWKTQMEE	88	43	IFLSFQHLLRGKVRF	116
16	FSLGEWKTQMEETKA	89	44	SFQHLLRGKVRFLML	117
17	GEWKTQMEETKAQDI	90	45	HLLRGKVRFLMLVGG	118

18	KTQMEETKAQDILGA	91	46	RGKVRFLMLVGGSTL	119
19	MEETKAQDILGAVTL	92	47	VRFLMLVGGSTLCVR	120
20	TKAQDILGAVTLLLE	93	48	LMLVGGSTLCVRRAP	121
21	QDILGAVTLLLEGVM	94	49	VGGSTLCVRRAPPTT	122
22	LGAVTLLLEGVMAAR	95	50	STLCVRRAPPTTAVP	123
23	VTLLLEGVMAARGQL	96	51	CVRRAPPTTAVPSRT	124
24	LLEGVMAARGQLGPT	97	52	RAPPTTAVPSRTSLV	125
25	GVMAARGQLGPTCLS	98	53	PTTAVPSRTSLVLTL	126
26	AARGQLGPTCLSSLL	99	54	AVPSRTSLVLTLNEL	127
27	GQLGPTCLSSLLGQL	100	55	SRTSLVLTLNELPNR	128
28	GPTCLSSLLGQLSGQ	101			

Please replace the paragraph beginning at line 1 on page 42 of the specification with the following amended paragraph:

-- The results of these assays are depicted in Figure 1. Regions of immunogenicity (Figure 1A) were determined by identifying peptides that induced donors to respond with stimulation indexes ≥2 and by determination of the donor response rate for each peptide. Peptides located within two separate regions were able to induce T cell proliferation. Region 1 encompasses TPO residues 49 – 75 and comprises the sequence: GEWKTQMEETKAQDILGAVTLLLEGVM (SEQ ID NO: 2) and equivalent to peptides 17 - 21. The donor responses to region 1 ranged from 13% to 17%. Region 2 encompasses TPO residues 157 – 171 and comprises the sequence: PTTAVPSRTSLVLTL (SEQ ID NO: 3) (peptide 53). The donor response rate to region 2 was 13% (Figure 1B). Each donor was also tested for their ability to respond to two positive control peptides influenza haemagglutinin A amino acids 307-319 [~~Krieger JI, et al (1991) *Journal of Immunology*; 146: 2331-2340~~ J. I. Krieger et al. (1991) *Journal of Immunology*; 146: 2331-2340] and chlamydia HSP60 amino acids 125-140 [~~Cerrone MC, et al (1991) *Infection and Immunity*; 59: 79-90~~ M. C. Cerrone et al. (1991) *Infection and Immunity*; 59: 79-90]. Keyhole limpet haemocyanin, a well documented potent T cell antigen was also used as a control. --

Please replace Table 4 beginning after line 12 on page 43 of the specification with the following amended table:

Immunogenic Region	Wild Type Sequence	Modified Sequences
R1	GEWKTQMEETK AQDILGAVTLL LEGVM (SEQ ID NO: 2)	GEWKTQKEETKAQDILGAVTLLLEGVM (SEQ ID NO: 129) GEWKTQMEERKAQDILGAVTLLLEGVM (SEQ ID NO: 130) GEWKTQMEETKRQDILGAVTLLLEGVM (SEQ ID NO: 131) GEWKTQMEETKAQRILGAVTLLLEGVM (SEQ ID NO: 132) GEWKTQMEETKAQDILGAVTALLEGVM (SEQ ID NO: 133) GEWKTQMEETKAQDILGAVTLALEGVM (SEQ ID NO: 134)
R2	PTTAVPSRTSL VLTL (SEQ ID NO: 3)	PTTAAPSRTSLVLTL (SEQ ID NO: 135) PTTANPSRTSLVLTL (SEQ ID NO: 136) PTTARPSRTSLVLTL (SEQ ID NO: 137) PTTATPSRTSLVLTL (SEQ ID NO: 138)